Amendments to the Claims:

Please cancel claims 10 and 15 without prejudice or disclaimer, please amend claims 1, 3-9, 11 and 12 and please enter new claims 49-53 as set forth in the complete listing of the claims below. The listing hereafter replaces all prior versions and listings.

1 (currently amended). A method for identifying a subject at risk of melanoma, which comprises detecting the presence or absence of one or more polymorphic variations associated with melanoma in a nucleic acid sample from a human subject, wherein the polymorphic variation is detected in an intron of a region between about the position of rs1267618 and about the position of rs1639679 ~~nucleotide sequence selected from the group consisting of~~

~~(a) the nucleotide sequence of SEQ ID NO: 1;~~

~~(b) a nucleotide sequence which encodes an amino acid sequence encoded by SEQ ID NO: 1;~~

~~(c) a nucleotide sequence which encodes an amino acid sequence that is 90% or more identical to the amino acid sequence encoded by SEQ ID NO: 1;~~

~~(d) a fragment of a nucleotide sequence of (a), (b), or (c); and~~

~~wherein the nucleotide sequence contains a thymine at position 171429 of SEQ ID NO: 1~~;

whereby the presence of the one or more polymorphic variations is indicative of the subject being at risk of melanoma.

2 (original). The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3 (currently amended). The method of claim 1, wherein the one or more polymorphic variations ~~is detected at~~ comprises a polymorphic variation at a site ~~position the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 1~~ selected from the group consisting of rs1639679, rs1267646, rs1267636, rs1639675,

rs1267649, rs1267609, rs1267625, rs1267601, rs1267606 and rs1267621 ~~146311, 138875, 132526, 128002, 118712, 98846, 98682, 87826, 80400, 76779, 68398 and 64547~~.

4 (currently amended). The method of claim 3, wherein the one or more ~~a~~ polymorphic variations comprises ~~is detected at~~ a rs1639679 polymorphic variation ~~position 146311 in SEQ ID NO:1~~.

5 (currently amended). The method of claim 3, wherein the one or more ~~a~~ polymorphic variations comprises ~~is detected at~~ a rs1267636 polymorphic variation ~~position 132526 in SEQ ID NO:1~~.

6 (currently amended). The method of claim 3, wherein the one or more ~~a~~ polymorphic variations comprises ~~is detected at~~ a rs1639675 polymorphic variation ~~position 128002 in SEQ ID NO:1~~.

7 (currently amended). The method of claim 3, wherein the one or more ~~a~~ polymorphic variations comprises ~~is detected at~~ a rs1267649 polymorphic variation ~~position 118712 in SEQ ID NO:1~~.

8 (currently amended). The method of claim 3, wherein the one or more ~~a~~ polymorphic variations comprises ~~is detected at~~ a rs1267609 polymorphic variation ~~position 98846 in SEQ ID NO:1~~.

9 (currently amended). The method of claim 3, wherein the one or more ~~a~~ polymorphic variations comprises ~~is detected at~~ a rs1267601 polymorphic variation ~~position 80400 in SEQ ID NO:1~~.

10 (cancelled).

11 (currently amended). The method of claim 3, wherein the one or more polymorphic variations comprises ~~is~~ the haplotype CTTG corresponding to rs1639679,

rs1267646, rs1267606 and rs1267621 positions ~~146311, 138875, 76779, and 68398~~, respectively~~, in SEQ ID NO: 1~~.

12 (currently amended). The method of claim 3, wherein the one or more polymorphic variations comprises ~~is~~ the haplotype ATGA corresponding to rs1639679, rs1267646, rs1267606 and rs1267621 positions ~~146311, 138875, 76779, and 68398~~, respectively~~, in SEQ ID NO: 1~~.

13 (original). The method of claim 1, wherein detecting the presence or absence of the one or more polymorphic variations comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of a polymorphic variation in the extension products.

14 (previously presented). The method of claim 13, wherein the oligonucleotide is selected from the group consisting of GTAATGTTGAAACTACAATTACCA (SEQ ID NO: 45); GAAACAGGCTTCAATTCATCTT (SEQ ID NO: 46); ACATAGAGGCAGGACTGTCA (SEQ ID NO: 47); ATTAGGACATGGCTGAGATATTCA (SEQ ID NO: 48); GGACTCTGCTTATTCTACCCA (SEQ ID NO: 49); AGAGATTGTGCTTCCCAAATC (SEQ ID NO: 50); GAATTAGTGAACTCTGGAAAGT (SEQ ID NO: 51); GAAATATGTTTGGAAAATTGTTCT (SEQ ID NO: 52); CTACAAAGCAAGACAGGACTAA (SEQ ID NO: 53); CCAAGATAAGAATCTGTTTTACC (SEQ ID NO: 54); AATGTTCTGAATTTTTCCAACTAA (SEQ ID NO: 55); and TTATAATTTAGTGGGGAACAGAA (SEQ ID NO: 56).

15-48 (cancelled).

49 (new). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267646 polymorphic variation.

50 (new). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267625 polymorphic variation.

51 (new). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267606 polymorphic variation.

52 (new). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267621 polymorphic variation.

53 (new). The method of claim 3, wherein the one or more polymorphic variations comprises a comprises a polymorphic variation at a site selected from the group consisting of rs1267649, rs1267609 and rs1267601.